0590
0417

#3

OIPE

ENTERED

RAW SEQUENCE LISTING   DATE: 04/23/2002 PM

PATENT APPLICATION: US/09/902,432   TIME: 15:29:06

Input Set : A:\09902432sequencelisting.txt
Output Set: N:\CRF3\04232002\I902432.raw

```
   3 <110> APPLICANT: Irwin H. Gelman
   4        Susan G. Jaken
   6 <120> TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
   9 <130> FILE REFERENCE: A30558-A-FWC-A 070156.0597
  11 <140> CURRENT APPLICATION NUMBER: 09/902,432
C--> 12 <141> CURRENT FILING DATE: 2002-04-08
  14 <150> PRIOR APPLICATION NUMBER: 08/978,277
  15 <151> PRIOR FILING DATE: 1997-11-25
  17 <150> PRIOR APPLICATION NUMBER: 08/665,401
  18 <151> PRIOR FILING DATE: 1996-06-18
  20 <150> PRIOR APPLICATION NUMBER: 08/635,121
  21 <151> PRIOR FILING DATE: 1996-04-19
  23 <160> NUMBER OF SEQ ID NOS: 35
  25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  27 <210> SEQ ID NO: 1
  28 <211> LENGTH: 5134
  29 <212> TYPE: DNA
  30 <213> ORGANISM: Rattus norvegicus
  32 <400> SEQUENCE: 1
  33 ggaaaagaca gagccagcct cggaggagca ggagccggca gaagacacag accaggccag 60
  34 gttgtcagca gactacgaga aggtggagct gcctttggaa gaccaggttg gtgacctgga 120
  35 ggcatcgtca gaggagaagt gtgctccttt ggcaacggaa gtgtttgatg agaagatgga 180
  36 agcccaccaa gaagttgttg cagaggtcca cgtgagcacc gtggagaaga cagaggagga 240
  37 gcagggagga ggaggagagg ctgaagggggg cgtggtggta gaaggaacag gagaatcctt 300
  38 gcccccctgag aaactggctg agccccagga ggtcccccag gaagctgagc ctgctgagga 360
  39 gctgatgaag agcagagaga tgtgtgtctc tggaggagac cacactcaac tgacagacct 420
  40 aagtcctgaa gagaagacgc tgcccaaaca cccagaaggc attgtcagtg aggtggagat 480
  41 gctgtcctct caggaaagaa tcaaggtaca gggaagtccc ttgaagaaac tcttcagtag 540
  42 ctcaggctta aagaagctgt ctgggaagaa gcagaagggg aaacgaggag gtgggggaga 600
  43 cgaagagcct ggagaatacc aacacattca caccgaatcc ccagagagtg ctgatgagca 660
  44 gaagggagag agctctgcgt cgtcccccga ggagcctgag gagaccacgt gtctggagaa 720
  45 agggccgctg gaagcaccca ggatggggaa gctgaggaag gaactacttc gtggagagaa 780
  46 gaagaggaag gatcactccc tgggcatcct tcaaaaagat ggtgacaccc aagaaacggt 840
  47 ccgaagacct tctgagagtg acaaggagga agagctggag aaggtcaaga gcgccacctt 900
  48 gtcctccact gatagcacag tgtcagaaat gcaagatgaa gtcaaaactg ttggtgagga 960
  49 acaaaagcca gaggaaccaa agcgtagggt ggatacttca gtgtcttggg aagcactgat 1020
  50 ttgtgtcgga tcatccaaga agagagcaag gaaggcatcc tcttcagata taagagggcc 1080
  51 aaggacactg ggaggggggac agtcacagag cagaggaggc cagcaaagac aaagaagccg 1140
  52 aacagacgct gttcctgcca gcacccagga gcaggaccaa gcgcaaggaa gttcctcacc 1200
  53 cgagccagcg ggaagccctt ccgaagggga aggtgtctcc acttgggagt catttaaaag 1260
  54 attagtcact ccaagaaaaa aatccaagtc aaaactggaa gagaaagaag ccggaaggac 1320
  55 tctagttgta ggagcaggtt gtccactgag atcgaaccgt gtagagaaga tcttgggtt 1380
  56 tccattaaga aattcatccc cggacggcgg aagaaaaggg cagatgggaa ggcaagaaca 1440
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 57 agccactgtg gaagactcag ggccagtgga gataaatgag gacgagcctg atgtcccagc 1500
 58 cgtcgtgcct ctgtctgagt atgatgcagt ggagagggag aagatggaag cccaggggaa 1560
 59 tgcggagctg cccagctgct ggggctgtgt agtgtccgag gagctcagta agactctggt 1620
 60 ccacactgtg agtgtcgcag tcattgatgg gaccagggca gtcaccagtg tcgaagagcg 1680
 61 gtctccttcg tggatatccg cttccgtaac agaacctctt gaacacacag cgggagaagc 1740
 62 catgccacct gttgaagagg tcactgaaaa agacatcatt gcagaagaaa ctcctgtgct 1800
 63 cacccagacg ttaccagagg gtaaagatgc ccatgacgac atggtcacca gtgaagtgga 1860
 64 tttcacctca gaagctgtga cagccacaga gacctcagag gctctccgta ctgaagaagt 1920
 65 taccgaagca tcgggggccg aagagaccac agacatggtg tccgcagttt cccagctgac 1980
 66 tgactcccca gacaccacag aggaagccac cccagttcag gaggtagagg gtggtgtgct 2040
 67 agatacagaa gaagaggagc gccagacgca ggccatcctc caagccgttg cagacaaggt 2100
 68 gaaagaggag tcccaggtgc ctgcaaccca gactgtgcag agaacggggt caaaagcact 2160
 69 ggagaaggtt gaggaggtag aggaggactc cgaagtgctg gcttcggaga aagagaagga 2220
 70 cgttatgccg aaaggacccg tgcaggaagc tggagctgag catcttgcac agggctctga 2280
 71 gactggacag gctactccag agagccttga agttcctgaa gtcacagcag atgtagacca 2340
 72 tgtcgccacg tgccaggtta tcaagctcca gcagctgatg gaacaggccg tggcccctga 2400
 73 gtcatccgaa accttgacag acagtgagac aaatggaagc actcccttag cagattcaga 2460
 74 cactgcagat gggacacagc aagatgaaac cattgacagc caggacagta aagccactgc 2520
 75 agctgtcagg cagtcacagg tcacagaaga agaggcggct actgctcaga aagaggagcc 2580
 76 ttcgacacta cctaataatg ttccagccca ggaagaacat ggggaagaac caggaagaga 2640
 77 tgttcttgaa cctacacagc aagagcttgc tgctgcagcc gtgcccgtct ggcaaaagac 2700
 78 tgaggtgggt caagagggtg aggttgactg gttggatgga gaaaaagtca aagaagaaca 2760
 79 ggaggtgttt gtacactctg gacccaacag tcaaaaggct gctgatgtga catatgacag 2820
 80 tgaagtgatg ggagtggccg ggtgtcagga aaaggagagt actgaagtgc agagtcttag 2880
 81 cctggaggag ggagagatgg aaactgacgt tgaaaaggag aaaagggaga caaagccaga 2940
 82 gcaagtgagt gaagaaggtg agcaggaaac agccgctcct gagcatgaaa ggaactacgg 3000
 83 gaagccagtc ctgacacttg acatgcccag ctcagagagg gggaaggcac tgggaagcct 3060
 84 tggaggaagc ccttctctcc cagaccaaga caaagcaggt tgcatagagg ttcaagttca 3120
 85 aagcctggac acaacagtca ctcaaacagc agaagctgtg gaaaaggtca tagaaacggt 3180
 86 tgtgatttca gagacaggtg aaagtccaga gtgtgtaggt gcacacttat taccagctga 3240
 87 gaagtcctct gcaacgggtg gccactggac tcttcagcat gcagaggaca cggtaccct 3300
 88 ggggcctgag tctcaggcag aatccatccc aatcatagta actcctgctc ctgaaagcac 3360
 89 cctacatcct gacctacaag gagaaataag cgcatcccag agagagcgat cagaggaaga 3420
 90 ggacaagcca gatgctggtc ctgatgctga cggcaaggag agtacagcaa tcgacaaagt 3480
 91 cctcaaggct gaacctgaga tcctggaact tgagagtaag agcaacaaga ttgtgctgaa 3540
 92 cgtcattcag acagccgttg accagttcgc acgtacagaa acagcccccg aaactcatgc 3600
 93 ttatgattca cagacccagg ttcctgcaat gcgcttggac agcagggagc ccaacagatg 3660
 94 ctggacaaaa atgaaagttg ccaagatgaa acacccagtg ccgcagccca gagaggactt 3720
 95 gcaagtcctg accgttctgg aggcatggct cagctcggaa atgcttgccg cgcttgcagt 3780
 96 tgaaagcgcc ggtgtcaaag taagcattga gaagctgcct cctcaacccca aagatcaaaa 3840
 97 ggagcatgct gctgatggcc ctcagctcca aagcttagcc caggcagagg cagtgtctgg 3900
 98 aaacctaacc aaagaatccc cagacaccaa cggaccaaag ctaaccgagg agcgatgccc 3960
 99 ccaaaagttg aggtccagga agaagaaatg tctaccaagt cagtcaaaga gaacaaggcc 4020
100 caggcagaag aggacctgca ggagccaaag ggagacctgg cagaatccta agatgttagt 4080
101 tgctcattgt acatctgtaa gaccagaatg tgaaaacaag tcacagaaca agatgctgct 4140
102 gttgggacct tggaccaaga tttcagagcc catgagatcc agagagcagg gccgtccaat 4200
103 gatttccacc cagtagagca ccccgacaat tctgaggctt catcgggagc tagagccagc 4260
104 taacatttcc tcgtttcaag actgcctttg atttgcccct tgatgccgtc cgtgtatttc 4320
105 taacatttcc tcgtttcaag actgcctttg atttgcccct tgatgccgtc cgtgtatttc 4380
```

RAW SEQUENCE LISTING   DATE: 04/23/2002
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Input Set : A:\09902432sequencelisting.txt
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```
106 ggatttaagg tcctgcgttc tcaacctgga accaattctg ccatacctag ttccacttct 4440
107 caaactggag catcctcctt tatgtattta tatgtatgtt ttatgtagtc ctcctcctgt 4500
108 acctattgta tatttttttc taacgtttaa gcacatgctt tttgtattat gcaatatata 4560
109 acgggtgtgc agccatagcg acgctttgaa aagctccaag cctcaactgt aacctgcagc 4620
110 aaacagataa cattcctggc aagaagagac aagtcttttt taaagtttac tgatgcttag 4680
111 atctgtgggc ttctagtcct ctgaaagtgg ttgttttcct atgcacagcg agctcagaaa 4740
112 taaaaacccc attttgaaac atccaggatg tcccaatatt accatgattt tttcccccct 4800
113 ttttgctaat ccagtccagg ttggaaagaa gtctcctctg tgtcagatta agccctgtct 4860
114 cttaatgata tggacaaatg agtgtgccta aggccatgag atgtttccta atgcagaagg 4920
115 aatctgttgt acgttttttt gattgtactc ttctatgctg gaccgaattc atatgcagat 4980
116 cgaagtgagt cctgttcttt acagatggta ttttgataga tactggagtt tgtctgtgtt 5040
117 atatctgtgc cccttcttta agaacaatgt tgcattatgt tcctttggat aaattgtgat 5100
118 ttgacaactg atttaaataa acatatttga ctac                               5134
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 1346
124 <212> TYPE: PRT
125 <213> ORGANISM: Rattus norvegicus
127 <400> SEQUENCE: 2
128 Met Glu Ala His Gln Glu Val Val Ala Glu Val His Val Ser Thr Val
129  1               5                  10                  15
130 Glu Lys Thr Glu Glu Glu Gln Gly Gly Gly Gly Glu Ala Glu Gly Gly
131             20                  25                  30
132 Val Val Val Glu Gly Thr Gly Glu Ser Leu Pro Pro Glu Lys Leu Ala
133         35                  40                  45
134 Glu Pro Gln Glu Val Pro Gln Glu Ala Glu Pro Ala Glu Glu Leu Met
135     50                  55                  60
136 Lys Ser Arg Glu Met Cys Val Ser Gly Gly Asp His Thr Gln Leu Thr
137 65                  70                  75                  80
138 Asp Leu Ser Pro Glu Glu Lys Thr Leu Pro Lys His Pro Glu Gly Ile
139             85                  90                  95
140 Val Ser Glu Val Glu Met Leu Ser Ser Gln Glu Arg Ile Lys Val Gln
141             100                 105                 110
142 Gly Ser Pro Leu Lys Lys Leu Phe Ser Ser Ser Gly Leu Lys Lys Leu
143         115                 120                 125
144 Ser Gly Lys Lys Gln Lys Gly Lys Arg Gly Gly Gly Gly Asp Glu Glu
145         130                 135                 140
146 Pro Gly Glu Tyr Gln His Ile His Thr Glu Ser Pro Glu Ser Ala Asp
147 145                 150                 155                 160
148 Glu Gln Lys Gly Glu Ser Ser Ala Ser Ser Pro Glu Glu Pro Glu Glu
149                 165                 170                 175
150 Thr Thr Cys Leu Glu Lys Gly Pro Leu Glu Ala Pro Arg Met Gly Lys
151             180                 185                 190
152 Leu Arg Lys Glu Leu Leu Arg Gly Glu Lys Lys Arg Lys Asp His Ser
153         195                 200                 205
154 Leu Gly Ile Leu Gln Lys Asp Gly Asp Thr Gln Glu Thr Val Arg Arg
155     210                 215                 220
156 Pro Ser Glu Ser Asp Lys Glu Glu Glu Leu Glu Lys Val Lys Ser Ala
157 225                 230                 235                 240
158 Thr Leu Ser Ser Thr Asp Ser Thr Val Ser Glu Met Gln Asp Glu Val
```

```
159                 245                 250                 255
160 Lys Thr Val Gly Glu Glu Gln Lys Pro Glu Glu Pro Lys Arg Arg Val
161                 260                 265                 270
162 Asp Thr Ser Val Ser Trp Glu Ala Leu Ile Cys Val Gly Ser Ser Lys
163             275                 280                 285
164 Lys Arg Ala Arg Lys Ala Ser Ser Ser Asp Ile Arg Gly Pro Arg Thr
165             290                 295                 300
166 Leu Gly Gly Gly Gln Ser Gln Ser Arg Gly Gly Gln Gln Arg Gln Arg
167 305                 310                 315                 320
168 Ser Arg Thr Asp Ala Val Pro Ala Ser Thr Gln Glu Gln Asp Gln Ala
169             325                 330                 335
170 Gln Gly Ser Ser Ser Pro Glu Pro Ala Gly Ser Pro Ser Glu Gly Glu
171             340                 345                 350
172 Gly Val Ser Thr Trp Glu Ser Phe Lys Arg Leu Val Thr Pro Arg Lys
173             355                 360                 365
174 Lys Ser Lys Ser Lys Leu Glu Glu Lys Glu Ala Gly Arg Thr Leu Val
175     370                 375                 380
176 Val Gly Ala Gly Cys Pro Leu Arg Ser Asn Arg Val Glu Lys Asn Leu
177 385                 390                 395                 400
178 Gly Phe Pro Leu Arg Asn Ser Ser Pro Asp Gly Gly Arg Lys Gly Gln
179             405                 410                 415
180 Met Gly Arg Gln Glu Gln Ala Thr Val Glu Asp Ser Gly Pro Val Glu
181             420                 425                 430
182 Ile Asn Glu Asp Glu Pro Asp Val Pro Ala Val Val Pro Leu Ser Glu
183             435                 440                 445
184 Tyr Asp Ala Val Glu Arg Glu Lys Met Glu Ala Gln Gly Asn Ala Glu
185     450                 455                 460
186 Leu Pro Ser Cys Trp Gly Cys Val Val Ser Glu Glu Leu Ser Lys Thr
187 465                 470                 475                 480
188 Leu Val His Thr Val Ser Val Ala Val Ile Asp Gly Thr Arg Ala Val
189             485                 490                 495
190 Thr Ser Val Glu Glu Arg Ser Pro Ser Trp Ile Ser Ala Ser Val Thr
191             500                 505                 510
192 Glu Pro Leu Glu His Thr Ala Gly Glu Ala Met Pro Pro Val Glu Glu
193             515                 520                 525
194 Val Thr Glu Lys Asp Ile Ile Ala Glu Glu Thr Pro Val Leu Thr Gln
195     530                 535                 540
196 Thr Leu Pro Glu Gly Lys Asp Ala His Asp Asp Met Val Thr Ser Glu
197 545                 550                 555                 560
198 Val Asp Phe Thr Ser Glu Ala Val Thr Ala Thr Glu Thr Ser Glu Ala
199             565                 570                 575
200 Leu Arg Thr Glu Glu Val Thr Glu Ala Ser Gly Ala Glu Glu Thr Thr
201             580                 585                 590
202 Asp Met Val Ser Ala Val Ser Gln Leu Thr Asp Ser Pro Asp Thr Thr
203             595                 600                 605
204 Glu Glu Ala Thr Pro Val Gln Glu Val Glu Gly Gly Val Leu Asp Thr
205     610                 615                 620
206 Glu Glu Glu Glu Arg Gln Thr Gln Ala Ile Leu Gln Ala Val Ala Asp
207 625                 630                 635                 640
```

```
208 Lys Val Lys Glu Glu Ser Gln Val Pro Ala Thr Gln Thr Val Gln Arg
209                 645             650             655
210 Thr Gly Ser Lys Ala Leu Glu Lys Val Glu Glu Val Glu Glu Asp Ser
211             660             665             670
212 Glu Val Leu Ala Ser Glu Lys Glu Lys Asp Val Met Pro Lys Gly Pro
213             675             680             685
214 Val Gln Glu Ala Gly Ala Glu His Leu Ala Gln Gly Ser Glu Thr Gly
215         690             695             700
216 Gln Ala Thr Pro Glu Ser Leu Glu Val Pro Glu Val Thr Ala Asp Val
217 705             710             715                         720
218 Asp His Val Ala Thr Cys Gln Val Ile Lys Leu Gln Gln Leu Met Glu
219             725             730             735
220 Gln Ala Val Ala Pro Glu Ser Ser Glu Thr Leu Thr Asp Ser Glu Thr
221             740             745             750
222 Asn Gly Ser Thr Pro Leu Ala Asp Ser Asp Thr Ala Asp Gly Thr Gln
223             755             760             765
224 Gln Asp Glu Thr Ile Asp Ser Gln Asp Ser Lys Ala Thr Ala Ala Val
225     770             775             780
226 Arg Gln Ser Gln Val Thr Glu Glu Glu Ala Ala Thr Ala Gln Lys Glu
227 785             790             795                         800
228 Glu Pro Ser Thr Leu Pro Asn Asn Val Pro Ala Gln Glu Glu His Gly
229             805             810             815
230 Glu Glu Pro Gly Arg Asp Val Leu Glu Pro Thr Gln Gln Glu Leu Ala
231             820             825             830
232 Ala Ala Ala Val Pro Val Trp Gln Lys Thr Glu Val Gly Gln Glu Gly
233             835             840             845
234 Glu Val Asp Trp Leu Asp Gly Glu Lys Val Lys Glu Glu Gln Glu Val
235         850             855             860
236 Phe Val His Ser Gly Pro Asn Ser Gln Lys Ala Ala Asp Val Thr Tyr
237 865             870             875                         880
238 Asp Ser Glu Val Met Gly Val Ala Gly Cys Gln Glu Lys Glu Ser Thr
239             885             890             895
240 Glu Val Gln Ser Leu Ser Leu Glu Glu Gly Glu Met Glu Thr Asp Val
241             900             905             910
242 Glu Lys Glu Lys Arg Glu Thr Lys Pro Glu Gln Val Ser Glu Glu Gly
243         915             920             925
244 Glu Gln Glu Thr Ala Ala Pro Glu His Glu Arg Asn Tyr Gly Lys Pro
245     930             935             940
246 Val Leu Thr Leu Asp Met Pro Ser Ser Glu Arg Gly Lys Ala Leu Gly
247 945             950             955                         960
248 Ser Leu Gly Gly Ser Pro Ser Leu Pro Asp Gln Asp Lys Ala Gly Cys
249             965             970             975
250 Ile Glu Val Gln Val Gln Ser Leu Asp Thr Thr Val Thr Gln Thr Ala
251             980             985             990
252 Glu Ala Val Glu Lys Val Ile Glu Thr Val Val Ile Ser Glu Thr Gly
253         995             1000            1005
254 Glu Ser Pro Glu Cys Val Gly Ala His Leu Leu Pro Ala Glu Lys Ser
255     1010            1015            1020
256 Ser Ala Thr Gly Gly His Trp Thr Leu Gln His Ala Glu Asp Thr Val
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/23/2002
PATENT APPLICATION: US/09/902,432   TIME: 15:29:07

Input Set : A:\09902432sequencelisting.txt
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 3,4,5,7,11,12,16,18,19,20
Seq#:21; Xaa Pos. 20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:21; Xaa Pos. 39,40,41,42,43,44,45,46
Seq#:22; Xaa Pos. 6,7,8,9

VERIFICATION SUMMARY   DATE: 04/23/2002
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L:12   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:812  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:816  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:820  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:824  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:828  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:832  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:836  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:840  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:844  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:848  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:849  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:851  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:16
L:881  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:16
L:883  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:32
L:900  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1049 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1053 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:1057 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
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